

GenCore version 5.1.4.D5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 00:17:03 ; Search time 2426.96 Seconds

(without alignments)
10930.628 Million cell updates/sec

Title: US-09-001-737-7_COPY_15_1652

Sequence: 1 ATGCGAACAATCAATTCATTT.....TGGGTGGATGGCGGATTA 1638

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estb:*
2: em_estb:*
3: em_estb:*
4: em_estb:*
5: em_estb:*
6: em_estb:*
7: em_estb:*
8: em_estb:*
9: em_estb:*
10: em_estb:*
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22: em_estb:*
23: em_estb:*
24: em_estb:*
25: em_estb:*
26: em_estb:*
27: em_estb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	471.8	28.8	2265	AY109623	AY109623 Zea mays
2	431.4	26.3	2290	AY104969	AY104969 Zea mays
3	430.6	26.3	2338	AY103778	AY103778 Zea mays
4	414.2	25.3	1327	BH770613	BH770613 LMKtag37
5	383.6	23.4	2143	AY108560	AY108560 Zea mays
6	302.8	18.5	1376	AY106465	AY106465 Zea mays

7	290	17.7	1387	AY108518	AY108518 Zea mays
8	263.2	16.1	887	CN5074DM	AL428672 Clone BAO
9	262.8	16.0	1090	BM799922	BM799922 AGENCOURT
10	261.8	16.0	878	BF275584	BE275584 GA_ED002
11	257.2	15.7	1035	AL518632	AL518632 AL518632
12	253.4	15.5	988	AL532233	AL532233 AL532233
13	253	15.4	977	BG312193	BG312193 Zm04_0490
14	251.6	15.4	955	AL515262	AL515262 AL515262
15	249.6	15.2	1017	AL515579	AL515579 AL515579
16	249	15.2	677	B1926411	B1926411 EST546300
17	248.6	15.2	810	BF267437	BF267437 HVSMBE000
18	248	15.1	959	AL557150	AL557150 AL557150
19	247	15.1	746	BU003474	BU003474 OGC35717
20	246.4	15.0	980	AL557181	AL557181 OGC35717
21	245	14.8	761	BO967821	BO967821 OGC35717
22	243	14.8	645	BM224051	BM224051 OGC35717
23	242	14.8	633	BU014013	BU014013 OGC35717
24	239.4	14.6	716	DA5006	DA5006 RICS10372A
25	237.6	14.5	657	AM223768	AM223768 EST300579
26	237.6	14.5	1119	BM458421	BM458421 AGENCOURT
27	236.2	14.4	668	AM398404	AM398404 EST298251
28	231.2	14.2	771	BF617440	BF617440 HVSMEC001
29	230.2	14.1	677	AV338920	AV338920 AGENCOURT
30	229.6	14.1	1051	BM478208	BM478208 OGC35717
31	228.8	14.0	744	BU000648	BU000648 OGC35717
32	227.4	13.9	680	AM330455	AM330455 PFOAF3
33	227.2	13.9	632	BG128308	BG128308 EST473954
34	226.6	13.8	650	AT432272	AT432272 AT432272
35	226	13.8	790	BE599254	BE599254 EST504154
36	226	13.8	1351	BE422296	BE422296 HMM022CF
37	225.6	13.8	895	BO216655	BO216655 AGENCOURT
38	225.4	13.8	946	BO882339	BO882339 AGENCOURT
39	225.4	13.7	709	AT486676	AT486676 EST244898
40	225.2	13.7	1016	BM450130	BM450130 AGENCOURT
41	224.8	13.7	739	BO915279	BO915279 OGC35717
42	224.4	13.6	744	BI176450	BI176450 EST511249
43	223	13.6	654	BI176450	BI176450 EST511249
44	222.4	13.6	660	BG354864	BG354864 MBTSMAL13
45	222.2	13.6	660	BG354864	BG354864 MBTSMAL13

ALIGNMENTS

RESULT 1
AY109623
LOCUS AY109623
DEFINITION Zea mays CU2221_1 mRNA sequence.
ACCESSION AY109623
VERSION AY109623.1 GI:21213414
KEYWORDS
SOURCE
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 2265)
Hainey/C.F., Dolan/M., Miao/G.H., Vogel/J.M., Whitesitt/M.S.,
Arthur/L.W., Hainey/M., Morigante/M. and Tingey/S.V.
Maize Mapping Project/Dupont Consensus Sequences for Design of
Overgo Probes
Unpublished (2002)
2 (bases 1 to 2265)
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
1..2265
/organism="Zea mays"
/db_xref="MaizeDB:630867"
/db_xref="taxon:4577"
/clone="CU2221_1"

/clone_11b-"Maize Mapping Project/Dupont Cornsensus
Library"
/note-"this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed Dupont contigs; this resource was
assembled by Dupont as part of a collaboration for the
overgo addressing of BACS in conjunction with the Maize
Mapping Project"

BASE COUNT 615 a 430 c 599 g 538 t 83 others
ORIGIN

Query Match 28.8% Score 471.8; DB 11; Length 2265;
Best Local Similarity 56.4%; Pred. No. 1.7e-120;
Matches 911; Conservative 0; Mismatches 694; Indels 9; Gaps 3;

OY 4 GCAAGAAATCAATTTTCAGCAGATGCCCTGCTGCCATGTCGCGAGTGTATG 63
DB 293 GCAAGAGCATCAATTTTCAGCAGATGCCCTGCTGCCATGTCGCGAGTGTATG 63
OY 64 TTAGCAGATACCTGCAAGTAAAGCTGCTCTTAAAGGCGCAATGTTCTTGA 123
DB 353 NNNNCAGATGCTCAAGTAAAGCTGCTCTTAAAGGCGCAATGTTCTTGA 123
OY 124 GCTTTGGTCTCCCTTAATTAATGACGGGTTMACCATTCCTAAAGATGAA 183
DB 413 AGCTTGGTGCAGAAATGTCANAAAGATGTTGATGACCAAGAGCATTTGAT 472
OY 184 GAAGATCATTTTGAAMACATGGAGCAAAATGTTGCTGTAAGTGGCTCTAA 243
DB 473 AAGGATAGATAAGAAATGTTGTCAGAGCTTGTGAACAGTTCTTAATGA 532
OY 244 GATATTCGTGATGAGGAGCAGTACTGACAGATTTGACACAAACCTTGTCA 303
DB 533 GACACTGCTGGCGATGTAACCATGTCCTGCTTTTGAACAAACATTTTACT 592
OY 304 GGACTAAATAATGTCAGAGAGCTGCTTAATCCAAATGTTGATCCGTGAGCA 363
DB 593 GGGTCAAAATCTTTGCGGCTGAGATGATGCAATGATTAAGGGGTGATGCA 652
OY 364 GCACAGCAACAGCTGTTGAAGCCTTGAAGCCATGTCACCTGATCTGCA 423
DB 653 GCTGTGACGCTGTTGTCACCATCTGAAGGACGCGAATGATGACATCTGA 712
OY 424 GCTATTCGTCGCTGCTGCAATCATCAGCTCTGAAA---AAGTTGAGATTA 480
DB 713 GAAATGTCAGAGTGGGTACAAATATCAGCAATGGGAAAGGAAATTTGTA 772
OY 481 TCAGAGCTATGAGGCTGTGGCAAGATGTTGATTCATTCATGGAAGATTC 540
DB 773 GCCAAGGCTATGAGAGTGGTGAAGAGGTTGTCATCTTTGCGAAGCTAAC 832
OY 541 ATGGAACAGACATCTGAAGTGTGAAGGATGCAATTTACCGTGTACTCA 600
DB 833 CTTTAAATAGCTTAAGATTTGAGAGGATGAAACACAGAGTAACTACTTC 892
OY 601 TACATGCTCAGACATGAAAAATGTTGCAACCTGTAAGAACCAATTTAT 660
DB 893 TACTTCATTAACCACTCAAAAGCCCAAGATGTAATTTGAAGAACCAAT 952
OY 661 ACGATTAATAAAGTGTCAACATTCAGACATTTTGCACACTACTTGAAG 720
DB 953 CATGACAAAGATTAACAAATATGATGCTGTGTTAAGTTTGAAGATGCTGA 1012
OY 721 ACGAACCCTCATTAATATGAGATGATGATGATGATGATGATGATGATG 780
DB 1013 AAACAAAGCCTCTACTGATGTTGCAAGATGGAAGATGGAAGATGGAAG 1072
OY 781 GCTTGAACAAGATGCTGATGATGATGATGATGATGATGATGATGATG 840
DB 1073 ATTAATGAAGCTGCTGCAAGATCAAGATGATGATGATGATGATGATG 1132
OY 841 GATGCTGATGAAGCTGATGATGATGATGATGATGATGATGATGATGAT 900

DB 1133 GAAACAGAGCAAGCAACTTACAGACCTTCAATCTTACTGAGAGATTAAT 1192
OY 901 GAGATGTAGAGCTTGAATTAAGATGCTCAATGACAGCCTTGGACGCTCTA 960
DB 1193 GAACACTGATTAACACTTGAATTTTGAAGCTTACATGCTGGGTATGCT 1252
OY 961 ATTAAGTGAATTAAGATTAACAGATTAATTTGAGTTGAGAGTTGAGAG 1020
DB 1253 GTGACTGTCTTAAGATGATGATGATGATGATGATGATGATGATGAT 1312
OY 1021 GCTAACGATTAATGATTAATGCAATTAATGAAACAAACATCTGATGAC 1080
DB 1313 GAAGAGGCGCAGACAGATTAATGATGATGATGATGATGATGATGATG 1372
OY 1081 GAAACACTAAGAACTTTGGCAAAATTAAGTGTGATGATGATGATGATG 1140
DB 1373 GAAAGCTCAGAGACGCTTGGCAAAAGCTCTGAGAGTGTGATGATGAT 1432
OY 1141 GCTCAACAGACAGCTTTAAAGAAATGAAATGAAATGCAATGATGATG 1200
DB 1433 GAGACAGCAAGCAAGATGATGATGATGATGATGATGATGATGATGAT 1492
OY 1201 ACAGTGCAGACGCTTGAAGAGATGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1493 ACTAAGCTGCTGTTGAAGAGATGATGATGATGATGATGATGATGATG 1552
OY 1261 ATTGAAGATGACAGCTCTGACCTG---AGCGATGATGCTACTGAGCA 1317
DB 1553 TCGAAGACCTGATTAATGTCAGACAGCACTTGAAGATGATGATGAT 1612
OY 1318 GTGCTGCTGCTGCTGCAAGAGCTTACCTCAATTTGATGATGATGATG 1377
DB 1613 ATTCAAAATGCTTTGAAGACACCTGTACACAAATGCTGATGATGATG 1672
OY 1378 TCCGATGATTAAGCAAG---TTGAAGAAACAGCCCTGCAAGAGATTA 1434
DB 1673 GCATGATGTTGAGAAAGCTTTTGAAGAGCAAGAAATGATGATGATG 1732
OY 1435 ACAGTGAAGTGTGATGATTAATTAAGAAAGATGATGATGATGATGATG 1494
DB 1733 AAGGTGAATATGTTGAACATGATGATGATGATGATGATGATGATG 1792
OY 1495 TCAAGCCTTCAAAATGAGCTCTGCTGATGATGATGATGATGATGATG 1554
DB 1793 AGCTGCTTGTGAGATGCTGCTGATGATGATGATGATGATGATGATG 1852
OY 1555 GCTAATTAACCTGAACCAAGCTACGACGCAAGCAATGCAAGAGTAT 1608
DB 1853 GTAGATATTCCAAGAGAGGACGCGCTCACGAATGAGTGTGCGATG 1906

RESULT 2
AY104969 2290 bp mRNA linear HTC 25-MAY-2002
LOCUS
DEFINITION
Zea mays PC0070942 mRNA sequence.
ACCESSION
AY104969
VERSION
AY104969.1 GI:21208047
KEYWORDS
HTC.
SOURCE
Zea mays.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 2290)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hainey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/Dupont Consensus Sequences for Design of
Overgo Probes
Unpublished (2002)
JOURNAL
REFERENCE
2 (bases 1 to 2290)
Coe,E.C.
AUTHORS
TITLE
JOURNAL
Submitted (25-Apr-2002) Maize Mapping Project, University of

FEATURES Missouri, Columbia, MO 65211, USA
Location/Qualifiers
Source 1. 2290
/organism="Zea mays"
/db_xref="MaizeDB:633867"
/db_xref="Laxon:4577"
/clone="PC0070942"
/clone_11b="Maize Mapping Project/Dupont Consensus Library."
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

BASE COUNT 684 a 457 c 583 g 565 t 1 others
ORIGIN

Query Match 26.3%; Score 431.4; DB 11; Length 2290;
Best Local Similarity 57.9%; Freq. No. 3.6e-109;
Matches 883; Conservative 0; Mismatches 622; Indels 19; Gaps 6;

52 GAGATTATGTTAGCAATACCTCAAGTAAAGCTTGTCTTAAAGCGGCAATGTT 111
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
426 GGGCTCAACAAGCTTGCATCTCGGGGTTACTTGGACCAAGGGGCAATGTA 485
112 GTTCTGAAAAGCTTTGTCTCCCTTAATTACTAATGACGGGTAACTTGCTAA 171
111 111 111 111 111 111 111 111 111 111 111 111 111 111
486 GTCTCGAACAACCAAGTATGCTCACTAAATGTAATGATGCTCACTGTGCAAG 545
172 GAGATGATATGAAATCATTTTGAATAAGTGGACAAATTTGGTCTGAAGTGGT 231
111 111 111 111 111 111 111 111 111 111 111 111 111 111
546 GAGGTGAACCTTGAGGCCCTCTTGAATAATTTGGTCAATTTGGTCCGCAAGCTGT 605
232 TCTAAACCATGATATGCTGATGATGAGGACATCTGCACATTTTGAACAGCC 291
111 111 111 111 111 111 111 111 111 111 111 111 111 111
606 GCTAAACCAATGACTGGCTGTGATGGGCAACCACTTGGTGTCTTCTTCAAGG 665
292 ATTGCTCATGAGACCTAAATAATGACAGCGGTATATCCATTTGATCCCTGCA 351
111 111 111 111 111 111 111 111 111 111 111 111 111 111
666 ATATCTACTAGGGGTGAAGGTGTACCTGCTGGTCAATGACGACATGCCGG 725
352 GCGATTGAACAGCACACAGCTGTGGAAGCTTGAAGCCCTTGAAGCTCTCAACGTGA 411
111 111 111 111 111 111 111 111 111 111 111 111 111 111
726 GGTATTGAGAAACGCAACGCAACCTAGTCAATGCAATGCAAGGAGGT 785
412 TCTGCAAGAAAGCTATTGCTCAGGTGCTGACATCATACCTCT...GAAAAAGTT 468
111 111 111 111 111 111 111 111 111 111 111 111 111 111
786 TGAGGACAGTACG...TTGCTGATGTTGCTGACAGTATGCGGGAATTAATATGAAT 843
469 GGAGATATATCTCAGAGCTATGAGCGGTGAGGCAAGATGATGATACATCGAA 528
111 111 111 111 111 111 111 111 111 111 111 111 111 111
844 GCGAATATGATAGCTAGGCTATGAAAAAGTTGGCGGAGGAGTGTACACTGAA 903
529 GAATCTCAGAGTATGGAACAGAACTTGAAGTGTGAAGGCAATGATGACCTGGT 588
111 111 111 111 111 111 111 111 111 111 111 111 111 111
904 GAAGGAAAGAGTCTGAAAAATACCTTATCTGTTGANGAATGCAATGTTGACCTGGC 963
589 TACGCTCTCATATGATGCTGACAGACAAAGAAAAAGTGTGCAACCTTGAACCCCA 648
111 111 111 111 111 111 111 111 111 111 111 111 111 111
964 TATATTCTCCCTCTTTGTGACACAGTGAAGAAAGACAGTCAATGATGAATGTC 1023
649 TTTATCTTAATACGATTAATAAAGTGTCAAAATCAACGATTTTGCACACTTGA 708
111 111 111 111 111 111 111 111 111 111 111 111 111 111
1024 AAGCTTCTCTCTGTCAGAAAGAAATTAACAATGCAAGATCTTATCAATCTTGA 1083
709 GAAGTCTTAATAACCAACCGCTCATCTACTATTTGATGATGATGATGATGATGATG 768
111 111 111 111 111 111 111 111 111 111 111 111 111 111
1084 GATGCTATTAATAGATGATATCAATTTCTAATAGGAGGAGCAATGATGAGGAGGCT 1143
769 CTTCACACCTTGTCTTGAACAAAGATTCGTGATCTTCAATGTGTTCTGTCGAAGCG 828
111 111 111 111 111 111 111 111 111 111 111 111 111 111
1144 CTTCACACCTTGTGCTTAATAGGCTTGAAGTCAATTTGAATGCTCTCTATTAAGGC 1203

Qy 829 CCAGATTTCGTATGCTGCTGAAGCTATGCTTGAAGCAATGCTATCTTGAAGCTGT 888
111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db 1204 CCTGATTTTGGAGAGCGCAAAAGTCAATATCTGATGATGATGATGATGATGATG 1263
889 ACAGTATTCAGAGGATCTAGCACTTGAATTAAGATGCTCAATCAATGACCGCTTGA 948
1264 ACTGTCATCAAGAAAGAGTGTATATCTTGAACAGGCAAGCAATGCGGCTTAGA 1323
Qy 949 CAGCTCTCAATGATGATGATTAAGATGACAGTATTTGATGATGATGATGATGAT 1008
111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db 1324 ACTGCTCTAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1383
Qy 1009 TCAGAACTTTCATACCGTATTCATGATGATGATGATGATGATGATGATGATGAT 1068
111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db 1384 CAGGAGAGTGAACAAAGGATGACAAATCAAGAACCAAGTGAAGTGAAGTGAAG 1443
Qy 1069 GACTTGAAGCTGAAAAACATCAAGAACGTTGGCAATTTAGCTGTGATGATGAT 1128
111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db 1444 GAAATATGAGGAAAAACATAAGAGAGATGATGATGATGATGATGATGATGATG 1503
Qy 1129 ATCAAACTAGAGCTCCAAAGAGACAGTGTAAAGAAATGAAATTCGATTTGAGAT 1188
111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db 1504 ATTCAGGTAGAGACAGACAGAACTGAGCTCAAGAAAGAAATGAGGTTGAGAT 1563
Qy 1189 GCTCAATATGCTACAGCTGACGCTGTTGAAGAGTATGCTGTGATGATGATGATGAT 1248
111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db 1564 GCGCTGATGCTCAAGAGCGAGAGCTGAGAGTATGATGATGATGATGATGATGAT 1623
Qy 1249 CTATATGCTGATTTGAAAAAGTAAAGACGCTTGAAG...CTTGAAGGAGTATGAT 1302
111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db 1624 CTATTGAGGTTGATCAAAAGTGAATGATGATGATGATGATGATGATGATGATG 1683
Qy 1303 AC...TGAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1359
111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db 1684 AAGCTTGGGCTGAAATGATGAGAAAGTCTGATGATGATGATGATGATGATGATG 1743
Qy 1360 AATCTGGGTCAGAAAGCTCCGATGATGATGATGATGATGATGATGATGATGATG 1415
111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db 1744 AATCTGGGTCAGAAAGCTCCGATGATGATGATGATGATGATGATGATGATGATG 1803
Qy 1416 AACGATTTAATGCTGACAGAGTATGATGATGATGATGATGATGATGATGATGATG 1475
111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db 1804 TATGGG...TACAAATGCGGCTACAGGAGATGATGATGATGATGATGATGATGATG 1862
Qy 1476 CCTGTCAAAGTAAACAGATCACGCTTCAAAATGACGCTGATGATGATGATGATG 1535
111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db 1863 TCCCAACCAAGTTGAGAGTGTGCTGATGATGATGATGATGATGATGATGATGATG 1922
Qy 1536 GACAACGAAGCAGTGTGCTAA 1559
111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db 1923 CACCTGATGATGCTGTGTGTA 1946

RESULT 3
AY103778
LOCUS AY103778 2338 bp mRNA linear HTC 25-MAY-2002
DEFINITION Zea mays PC0063180 mRNA sequence.
ACCESSION AY103778
VERSION AY103778.1 GI:21206856
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Halaney, C.E., Dolan, M., Miao, G.H., Vogel, J.M., Whitesitt, M.S.,
Arthur, L.W., Hanley, M., Morgante, M., and Tingey, S.V.
TITLE Maize Mapping Project/Dupont Consensus Sequences for Design of
Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 2338)

Db 571 GGGCATGTTGACATTAATCTTCAAGGCGCAATCCAGTGTCCGTTAGAAAGGCGATTGATA 630
 Oy 363 AGCAGACGACACAGCTGTGTAAGCCCTTGAAAGCCATTGCTCAACCTGTATCTGGCAAGA 422
 Db 631 GACTGTTCAAGAAATTTGGTGGAGAACCTTGAGAAATAATCAAGCCGCTCAAGGCTAGTGG 690
 Oy 423 AGCTATTGCTCAGTCCCTGCTGATATCATACGCTGTGAAAAGTTGGAAGATAT---AT 479
 Db 691 GGAATATTAAAGCTGTGTGCTCCATATCAGTGTGAATATGAAATTTGTGGGCAATATAT 750
 Oy 480 CTCAGAACTATGAGCGGTGTGGGCAAGATGTGGATATACCATGCAAAATATCCGAG 539
 Db 751 CGCCGAAAGCTATGTCAGAAAGTTGGCCCTGATGGTGTCTTCATATGATGCTCATGCTC 810
 Oy 540 TATGAAACAGACGCTGAAGTGTGTAAGGATGCAATTTGACCGTGTACCTGTCTCA 599
 Db 811 GTTGAAGACACAGTTGAAGTTGAAGAGGATGAGCTTGACAGAGGATATATCTCCCC 870
 Oy 600 ATACATGCTCACAGACATGAAAAATGTTGCAACCTTGAAACCCATTATCTTAT 659
 Db 871 TCAATTTGCTCACTTAACCTTGAAAAATCTATTGTGAGTTCGAAATCTCGATTTCTTGT 930
 Oy 660 CACGATTAAGAAAGTGTCAAAACATCAAGACATTTTCCACTACTTGAGAGATCTTAA 719
 Db 931 CACTGATCAGAAAGATATCATGATTAAGAAATTTATCTCTGTTGGAGCAGACACACA 990
 Oy 720 AACCAACGCTCATTAATTAATTTGACATGATGTGATGATGTAAGCACTTCAACCT 779
 Db 991 GTTAAAGACACCTTCTTATTAATGACAGAGATGTAAGTGGCGAGCGCTGCAACAT 1050
 Oy 780 TGTCTTGAACAAGATGTGTGACTTCAATGTGTGTGCTGCAACCGCGAGATTTGG 839
 Db 1051 AGTCATAAACAAGCTGTGAGAGAAATTTAAATGTGGCTGATCAAAAGCTCGCTTTGG 1110
 Oy 840 TGATCGTGTAAAGCTGTGAGAGATTTGATCTACTGACAGGATGATGATGATGAT 899
 Db 1111 TGAGAGGCTAAAGCTCTTCTCAAGACATTTGCAAGCTGTCAAGCTGTCAATG 1170
 Oy 900 AGAGATCTAGAGATTTGAATTAAGATGCTAATGACACCTTGGACAGCTGCTAA 959
 Db 1171 CAAGATCTGTGTCTACTGATGATGATGATGATGATGATGATGATGATGATGAT 1230
 Oy 960 GATTAAGTGTATTAAGATGACAGATTAATGTTGTAAGTTGCAAGATTTGCAAGCT 1019
 Db 1231 AGTTCAATCTCAAGTTCTCTGAGACCATTAATGAGATCTCTGAGCAAGAGATAT 1290
 Oy 1020 TGTAAACGATTTGCACTGATTAATGCAATTAAGAAACAACTTGTACTTGTACCG 1079
 Db 1291 CCAGGCCAGAAATCGCCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1350
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 Oy 1140 AGCTCCACAG 1199
 Db 1411 AGCATCGACGAG 1470
 Oy 1200 TACAGTGCAG 1259
 Db 1471 GACTTTTGCAGCAATGAG 1530
 Oy 1260 TATTGAAAAAGTACAGCTCTTGAGCTTGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1310
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 Oy 1311 TAACATTTGCTTCTGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1370
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 Oy 1371 CGAAGCTCCGATGATTAATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1430
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Oy 1431 TGCAGAGTGTAGTGGTTGATATGATTAAGAGAGATATGACCTGTCAAGTAC 1490
 Db 1711 CATGGCGACACAGACAGAGAACTGTGAGAGCTGTGTATGATGACCTGTCAAGTAC 1770
 Oy 1491 AGCATCACCTCTCAAAATGCAAGCTTCTGTACCTAGTCTTATTTGACACAGAGCACT 1550
 Db 1771 TAGGTGCGCCCTCTCAAGAGAGCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGT 1830
 Oy 1551 TGTCTTAATTAAGTGAAG 1610
 Db 1831 CTTGTGAG 1890
 Oy 1611 AGGAATGATG 1620
 Db 1891 TTTCAACATG 1900

RESULT 6
 AY106465 1376 bp mRNA Linear HTC 25-MAY-2002
 LOCUS AY106465
 DEFINITION Zea mays PC0128697 mRNA sequence.
 ACCESSION AY106465
 VERSION AY106465.1 GI:21209543
 KEYWORDS HTC.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 1376)
 Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitesitt, M.S.,
 Arthur, J.W., Hainey, M., Morgante, M. and Tingey, S.V.
 Maize Mapping Project/Dupont Consensus Sequences for Design of
 Overgo Probes
 Unpublished (2002)
 2 (bases 1 to 1376)
 Coe, E.C.
 Direct Submission
 Submitted (25-APR-2002) Maize Mapping Project, University of
 Missouri, Columbia, MO 65211, USA
 location/Qualifiers
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 /organism="Zea mays"
 /db_xref="taxon:4577"
 /clone="PC0128697"
 /clone_1kb="Maize Mapping Project/Dupont Consensus
 Library."
 /note="this sequence is part of a project of EST
 assemblies resulting from the application of public
 contigs to seed Dupont contigs; this resource was
 assembled by Dupont as part of a collaboration for the
 overgo addressing of BACs in conjunction with the Maize
 Mapping Project."
 BASE COUNT 397 a 277 c 359 g 343 t
 ORIGIN

Query Match 18.5% Score 302.8; DB 11; Length 1376;
 Best Local Similarity 55.7% Pred. No. 2,8e-73;
 Matches 621; Conservative 0; Mismatches 487; Indels 6; Gaps 2;
 Oy 464 AAGTGGAGAGATATCTCAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 523
 Db 23 AATTTGAGATCTAATATCAAAAGCATGCAAAAGTTGGAAGAGATGAGATCTATTA 82
 Oy 524 TCGAAGAACTCGAGAGATGAGAAACAGAACTGAAAGTGTGAAGAGAGAGAGAGAGAG 563
 Db 83 TTGTGATGCAAAACATGAGACATGAGCTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 142
 Oy 584 GTGTTTACTGTCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 643
 Db 143 GAGATACATATCTCTTACTTGTGACTGATCAAAAGACTCAGAAATGTGATGAGAGAG 202

QY 644 ACCCATTTATCTTAATCAGGATAAAGATGTCACATCCAGACATTTGGCAGCTAC 703
 DB 203 ACCCTTATCTTAATCAGGATAAAGATGTCACATCCAGCTAC 262
 QY 704 TTGGAGAAAGTCTTAACACACCGCTTACATCTTAATGATGATGATGATGATG 763
 DB 263 TAGAAATTTCTTAACACACCGCTTACATCTTAATGATGATGATGATGATG 322
 QY 764 AAGCATCTTCAACCTTCTGATGATGATGATGATGATGATGATGATGATGATG 823
 DB 323 ATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 382
 QY 824 AAGCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 883
 DB 383 AAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 442
 QY 884 GTGCTACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 943
 DB 443 GAGAGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 502
 QY 944 TTGGACAGGCTCTAAGATTAACAGTTGATTAAGATTAACAGTTGATTAAGATTA 1003
 DB 503 TTGGACAGGCTCTAAGATTAACAGTTGATTAAGATTAACAGTTGATTAAGATTA 562
 QY 1004 GAATTCAGAGCTATTTGCTACCGTATGCTATGCTATGCTATGCTATGCTATG 1063
 DB 563 GTGACAAACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 622
 QY 1064 CTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1123
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 QY 1124 CTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1183
 DB 683 CTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 742
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 DB 863 AGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 922
 QY 1361 ATGCTGAGGATTAACAGTTGATTAAGATTAACAGTTGATTAAGATTAAGATTA 1417
 DB 923 ATGCTGAGGATTAACAGTTGATTAAGATTAACAGTTGATTAAGATTAAGATTA 982
 QY 1418 CAGGATTTAATGCTGACAAAGTGTGATGATTAATTAAGATTAAGATTAAGATTA 1477
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 DB 1103 CACAGAGAGCTTTGCTAATAAAGCTGAGC 1136

SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 Gladii; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 1387)
 AUTHORS Halvey, C.F., Dolan, M., Mao, G.H., Vogel, J.M., Whitsitt, M.S.,
 Halvey, L.W., Hanley, M., Morgante, M., and Tingey, S.V.
 TITLE Maize Mapping Project/Dupont Consensus Sequences for Design of
 Overgo Probes
 JOURNAL Unpublished (2002)
 REFERENCE 2 (bases 1 to 1387)
 AUTHORS Coe, E.C.
 TITLE Direct Submission
 JOURNAL Submitted (25-Apr-2002) Maize Mapping Project, University of
 Missouri, Columbia, MO 65211, USA
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 /organism="Zea mays"
 /db_xref="maizedb:537188"
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 /clone="PCO123570"
 /clone_1ib="Maize Mapping Project/Dupont Consensus
 library."
 /note="This sequence is part of a project of EST
 assemblies resulting from the application of public
 contigs to seed Dupont contigs; this resource was
 assembled by Dupont as part of a collaboration for the
 overgo addressing of Bacs in conjunction with the Maize
 Mapping Project."
 BASE COUNT 426 a 257 c 332 t
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 Query Match 17.7%; Score 290; DB 11; Length 1387;
 Best Local Similarity 56.0%; Pred. No. 1,1e-69;
 Matches 593; Conservative 0; Mismatches 455; Indels 10; Gaps 2;

QY 554 TTGAAGTGGTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 613
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 QY 614 ACAAATGAAAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 673
 DB 74 ACGTGAAATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 133
 QY 674 TGTCAATGCAAGCATTTGCTGATGATGATGATGATGATGATGATGATGATGATG 733
 DB 134 TGTCAATGCAAGCATTTGCTGATGATGATGATGATGATGATGATGATGATGATG 193
 QY 734 TACTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 793
 DB 194 TGTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 253
 QY 794 TTGCTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 853
 DB 254 TTGCTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 313
 QY 854 CTATGCTGAAAGCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 913
 DB 314 CTATGCTGAAAGCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 373
 QY 914 TTGAATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 973
 DB 374 TGTGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 433
 QY 974 AAGATGACAGATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATG 1033
 DB 434 AAGATGACAGATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 493
 QY 1034 CAGCTGATTAATGCAATTAAGAAACAACTGATGATGATGATGATGATGATGATGATG 1093
 DB 494 CAGCTGATTAATGCAATTAAGAAACAACTGATGATGATGATGATGATGATGATGATG 553

RESULT 7
 AY108518 1387 bp mRNA linear HTC 25-MAY-2002
 LOCUS Zea mays PCO123570 mRNA sequence.
 DEFINITION
 ACCESSION AY108518
 VERSION AY108518.1 GI:21211596
 KEYWORDS HTC.

QY 1094 AACCTTGGCGAAATTAAGCTGTGTAGCTTTATCAAAAGTAGAGCTCAACAGAGA 1153
 DB 554 AGAATTTGCTAAAGCTTGGCGGTGGTGTCTTATCAAAAGTTAGAGCTCAACTAGAGA 613
 QY 1154 CAGCTTTAAAGAAATGAATTCAGATTGAGATGATTAATGCTACAGCTGACCGCG 1213
 DB 614 CTGAGCTTGAAGAGCCGACCTTAAGATTGAGATGATGAAAAAATCCACTTTGCAAGCTA 673
 QY 1214 TTGAAGAGATGCTGT 1264
 DB 674 TAGAGAGGAGCATTTGTCAGAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 733
 QY 1265 AAAAGTAGACCTTTGAGCTTGAAGGCGATGATGCTACGTGAGATGATGCTTTC 1324
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 QY 1335 GTGCTCTAGAGAGCTGTGCTGCTCAATTTGCTTAATCTGAGGAGAGCTCCGTAAG 1384
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 QY 1385 TTATGACAAAGTTGAA-AAACAGCCCTGCAGAGAACAGATTTAACTGTCAGACAGTGA 1443
 DB 854 TTGTGAGAAAGATCAAGGAGAGGATTTGGAGGAGTGGCTTACATGCAATGACATGACA 913
 QY 1444 TGGGTTGATGATGATTTAAACAGAAATCATTTGACCTGCTCAAGTACAGATGACGCTT 1503
 DB 914 TACGAGAACCTGATGAGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 973
 QY 1504 CAAATGACAGCTTCTGAGTGTGCTTATTTTGAACAAGAGAGTGTGTGTGTGTGTGT 1563
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 DB 1034 CCAAGCGCAAGCTCAAGTGTGCAAGGCAAGCGAGAG 1071

RESULT 8 887 bp DNA linear GSS 07-JUL-2001
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 LOCUS clone BA08027B07 of library BA0AB from strain CLIB 210 of
 DEFINITION Kluveromyces lactis, genomic survey sequence.
 ACCESSION AL428672
 VERSION AL428672.1 GI:12211866
 KEYWORDS GSS.
 SOURCE Kluveromyces lactis.
 ORGANISM Kluveromyces lactis.
 REFERENCE 1 (bases 1 to 887)
 AUTHORS Souciet,J.L., Aigle,M., Attguenave,F., Blandin,G.,
 Bolotin-Fukuhara,M., Bon,E., Brotier,P., Casaregola,S.,
 de-Montigny,J., Dujon,B., Duren,P., Lepingle,A., Llorente,B.,
 Malpertuy,A., Neuvéglise,C., Ozier-Kalogiropoulos,O., Potier,S.,
 Saulin,M., Tekala,F., Toffano-Nioche,C., Weslowski-Louvel,M.,
 Winkler,P. and Weissenbach,J.
 TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
 yeast species for molecular evolution studies
 JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
 MEDLINE 20584711
 PUBMED 11152876
 REFERENCE 2 (bases 1 to 887)
 AUTHORS Bolotin-Fukuhara,M., Toffano-Nioche,C., Attguenave,F.,
 Duchateau-Nguyen,G., Lemaire,M., Marmessier,R., Montrocher,R.,
 Robert,C., Termier,M., Winkler,P. and Weslowski-Louvel,M.
 TITLE Genomic exploration of the hemiascomycetous yeasts: 11.
 JOURNAL FEBS Lett. 487 (1), 66-70 (2000)
 MEDLINE 20584721
 PUBMED 11152886
 REFERENCE 3 (bases 1 to 887)
 AUTHORS Genoscope.
 TITLE Direct Submission

JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage,
 2 rue Gaston Crémieux, CP 5706, 91057 Evry cedex, FRANCE. (E-mail :
 seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 COMMENT This GSS is part of a random genomic sequencing program of thirteen
 yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
 kluyveri, Saccharomyces servazzii, Zygosaccharomyces rouxii,
 Saccharomyces kluyveri, Kluveromyces marxianus var. marxianus,
 Kluveromyces lactis var. lactis, Kluveromyces thermotolerans, Kluveromyces
 angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
 Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
 5 kb were prepared and both extremities were sequenced. See
 keywords for description of this sequence and for the sequence of
 the other extremity of this insert.
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 /db_xref="taxon:28985"
 /clone="BA08027B07"
 /clone_id="BA0AB"
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 HSP60 : heat shock protein - chromosome, mitochondrial |"
 /evidence="not-experimental"
 BASE COUNT 256 a 163 c 216 g 252 t
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 Best Local Similarity 58.78; Pred. No. 2.7e-62;
 Matches 493; Conservative 0; Mismatches 343; Indels 4; Gaps 2;
 QY 7 AAGAAATCAATTTTACAGATGCGCGTGTGCAATGCTGCGGAGATTGATGTA 66
 DB 25 AAGAAATCAATTTTACAGATGCGCGTGTGCAATGCTGCGGAGATTGATGTA 66
 QY 67 GCAGATACCGCTCAAGTAACCTGTGTCTTAAGAGGCGCAATGTTCTTGAAGAGT 126
 DB 85 GCGAGAGCTGTTTCTGCGCATTGGGCTCCAAAGAGTGAAGCTTTGATGACACCA 144
 QY 127 TTGGTCTCTCCCTTAATTAATGACGGGTAACCAATCTGTAAGAGATGATGTA 186
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 QY 187 GATCATTTTGAAGATGAGGAGCAAAATGCTGCTGAAGTGTCTTAACCATGAT 246
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 DB 265 GCTGCGGTGAGGATGACCACTTGTGCAACAGTTTGAAGGCGCATTTGCACTGAATCC 324
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 DB 385 GTCGAAAAAATTAATCAATTAATGTCAGAGAAACAAGAAAGAAATCAACACTGTGCTGA 444
 QY 427 ATTGCTAGGTGCTGCTGAGTATCATC---AGCTCTGAAGAAAGTGAAGTATATCA 483
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 QY 484 GAAGCTTGAAGCGTGTGCGACAGATGCTGATTAACATGGAAGATCTCAAGATATG 543
 DB 505 TCAGCTGGAAGAAAGTTGTGAAGAGGATGATCACTATGAGAGGAGATCAACCTTG 564
 QY 544 GAACAGACTGAAGTGTGAAGCATGCAATTTGACCGGTGATCACTGCTCAATAC 603
 DB 565 GAAGTAATGAAGTCACTGAGAGGTATGAGATTCACCGGTGATCACTTCTCCATAC 624
 QY 604 ATGTCACAGACAAATGAAGAAATGTTGAGACCTTGAAACCAATTAATCAACAG 663


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Db 625 TTATATACGACGCTAAATCTGTAGAGTGATTTGAAAACCTTTGATCTTATATAGT 684
Oy 664 GATAAAAAGTGTCAAAACATCCAAACATTTTCCGCTACTGTGAGAAAGTTTAAACC 723
Db 685 GAAAGAAAGATCTCTCATCCAGATATCTCTCTCTTTGGAATTTGCAAAACCAAC 744
Oy 724 ACCCTTCATTCATCATTTATGAGATGATGTGATGAGCACTTCCAAACCTTGTG 783
Db 745 AGAAGCACTGTGTGATCATGCCGGAAGATATTGATGCG-ACCTTGGCTCTGTATT 803
Oy 784 TTGAACAGATTCGTGTACTCTTCAATGTGTGCTGTCAAGCGCCAGAGATTGTAT 843
Db 804 TTGAACAGATTCAGAGTCAGTTCAAGTTGTGCGCTTAAAGCTCCAGTTTGGTGAT 863

RESULT 9
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LOCUS AGENCOURT.6417164 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5492101
DEFINITION 5' mRNA sequence.
ACCESSION BM799922
VERSION BM799922.1 GI:1916745
KEYWORDS EST
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1090)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM2113 row: k column: 14
High quality sequence stop: 743.
Location/Qualifiers
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/organism="Homo sapiens"
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/lab_host="DH10B (phage-resistant)"
/notes="Organ: eye; Vector: pCMV-Sport6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
BASE COUNT 332 a 209 c 274 g 275 t
ORIGIN
Query Match 16.0% Score 262.8; DB 14; Length 1090;
Best Local Similarity 56.2% Pred No 4e-62;
Matches 514; Conservative 0; Mismatches 397; Indels 3; Gaps 1;

Oy 4 GCAAAAGATCAATTTTCAGCAGATGCGCTGCTCCATGTCGCGCAGATTATATG 63
Db 122 GCCAAGATGTAATAATTTGGTCAGATGCCCACTTAATGCTTAAGGTGTAGACCTT 181
Oy 64 TTAGCAGATACCGTCAAAAGTACGTTGTCTTAAGCGCGCAATGTGTTCTGAATAA 123
Db 182 TTAGCGGATGCTGTGCGCTTACATGCGGCAAGGAGAAACATGATATTATGACAG 241
Oy 124 GCTTTGGTTCCTCTTAATTAATGACGGGTAAACCATCTCTTAAGAGATGCAATTA 183
Db 242 AGTTGGGAGAGTCCCAAGATGATGCTGTGCTCAAGATCAATTGACTTA 301

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Oy 184 GAAATATTTTGAACACAGGACCAAAATTTGTCTGAGTGGCTTCAAAACAT 243
Db 302 AAAGATTAATACAAACAAACATTTGAGCTTAACCTTGTCAAGATTTGCCAATCAACAAAT 361
Oy 244 GATATTCGTGGTATGAGGAGACTACTGCAACAGTTTTCACAAAGCCATTGTTCATGA 303
Db 362 GAAAGACCTGGGAGATGGGACTACCACTGCTACTGTACGACGCTCTATFAGCAAGGA 421
Oy 304 GGACTAAATAATGTACACAGAGTGTATCCATTTGATCGTCGAGCATTTGAACA 363
Db 422 GCGTTTCAGAGATTTAGCAAAAGGTGCTATCCATGGAATCAGAGAGGTGTGATGTA 481
Oy 364 GCACACAGCAACAGCTTTGAAAGCTTGAAGCCATTTGCTCAACCTGTATCGCAAGGA 423
Db 482 GCTGTATGCTGTATTTCTGCACTTAATAAGCACTTAAGCACTGTACACCTGTA 541
Oy 424 GCTATTCCTAGTGGCTGCGCATGATCATCAGCTCTGAAAAG---TTGAGAGATATC 480
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Oy 481 TCAGAACCTATGAGACGCTGTGGCAACGATGCTGTATTCATGAGAAATCTCGAGT 540
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Db 662 CTGAATGATGAATTTGAATTTATTTAGGACATGAAGTTTGATGAGGCTATATTCTCCA 721
Oy 601 TACATGCTCAGCAATGAAAAATGTTGCACACCTTGAAGAACCCATTACTATATC 660
Db 722 TACTTATTATATACATCAAAAGCTCGAATATGTAATTCAGATGCTATGTCTGTG 781
Oy 661 AGGATTAATAAGTGTCAACATCCCAACATTTTGGCACTCTTGAGAAATGTTCTAA 720
Db 782 AGTAAGAAAGAAATTTCTAGATATCCAGTCTGCTGCTTGAATTTGCCACTCT 841
Oy 721 ACACACCGTCAATTCATATTTATGCAATGATGATGATGAGCACTTCAACCTT 780
Db 842 CACGTACCTCTTGTCTATTAATCCGTAAAGATGATGAGAGCACTTCAATCACTC 901
Oy 781 GCTTGACAGAAATTCGTGTACTTCAATGTGTGCTGTCAAGCCGCGAGATTGGT 840
Db 902 GTCTTAATAAGGCTTAAGAGTGTCTCCAGGCTGTGCAAGCTCAGGGTTTGTG 961
Oy 841 GATGCTGCTAAGCTATGCTTGAAGACATTTCTATCTTGCAGGTGTAGATGATGCA 900
Db 962 GACAAATAGAAACACAGCCTTAAGATATGCTATTTGCTATGCTGTGGCGCAAGTTTG 1021
Oy 901 GAGGATCTAGGACT 914
Db 1022 GAAAAAAGGAT 1035

RESULT 10
BP275584 878 bp mRNA linear EST 07-MAR-2001
LOCUS GA_EB0024G33f Gossypium arboreum 7-10 dpa fiber library Gossypium
DEFINITION Arabidopsis cDNA clone GA_EB0024G33f, mRNA sequence.
ACCESSION BP275584
VERSION BP275584.1 GI:11206654
KEYWORDS EST.
SOURCE Gossypium arboreum.
ORGANISM Gossypium arboreum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eustosids II; Malvales; Malvaceae; Gossypium.
REFERENCE 1 (bases 1 to 878)
AUTHORS Wang, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry
D., Wood, T.C., Leslie, A. and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
JOURNAL Unpublished (2000)

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Db 296 AAGATTAATACAAAACATGAGCTAAAGTGTGTCAGATGTTGCCAATACACAAAT 355
Oy 244 GATATTCGTGATGGAGAGCTACTGCAACACTTTTGACACAAAGCATTTGTCATGA 303
Db 356 GAAAGACCTGGGATGGACATACCATCTACTGCTACTGCTCTATAGCCAGGAA 415
Oy 304 GACTAATAAAATGTACAGCAGGTGCTATTCATTTGTTCCGTGAGCATTTGAACA 363
Db 416 GCTTCGAGAAAGTTGCAAAAGGCTGTAACCTGTAAGATGAGAGGCTGATGATTA 475
Oy 364 GCACACGCAACAGCTGTTGAAGCCTTGAAGCCATGCTCAACCTGATCTGGCAGNAA 423
Db 476 GCTGTATGCTGTATGATGCTGAACCTTAAAGACAGCTTAAACCTGTACCCCTGAA 535
Oy 424 GCTATGCTGAGTGTGCTGAGTATCATCAGCTCTGAAAAAG---TTGAGAGTATATC 480
Db 536 GAAATTCACAGAGTGTGCTAGCATTTCTGCAACGAGACGAAAGAAATTTGCAATATC 595
Oy 481 TCAGAACCTATGAGAGCTGTGGCAGACAGTGTGTGATTCATGGAATCTGAGGT 540
Db 596 TCTGATCATATGAAAAAGTTGGAAGAAAGGCTGCTATCAGTAAAGATGAAAAACA 655
Oy 541 ATGGAACAGAACTGGAAGTGTGGAAGCATGGAATTTGACCGGTGTTACCTGCTCA 600
Db 656 CTGAATGATGAATTTGAAATTTATTTAGAGCATSCCGTTGATCGAGCTATATTTCTCA 715
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Db 716 TACTTTATTAATACATCAAAAGGTCAGAAATGTAATTCAGATGCTTATGTTCTGTG 775
Oy 661 ACGGATAAAAAGTGTCAACATCCAGACATTTTGCCACTACTGTGAGGAATTTCTTAA 720
Db 776 AGTAAAAAGAAATTTTACATGTCAGTCACTTACCTGCTTGAATTTGCCATCT 835
Oy 721 ACGAACGCTCATCTTACTATTTAGCATATGATGATGATGATGAGACCTTCCACCTT 780
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Oy 781 GCTTTGAAAGATGCTGCTGCTACTTCAATGTTGCTGTGCTGAAAGCCAGGATTTGT 840
Db 896 GCTTGAATAGGCTTAAAGTTGCTTTCAGGTTGTGCAAGTGTGCAAGGCTCAGGAGTTGG 955
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Db 956 TGCATATGATGAGAACGCTTAAAGTATGCTTATGCTTACGTTGT 1003

RESULT 12
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DEFINITION AL532233 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DM004YH20 5
prime, mRNA sequence.
ACCESSION AL532233
VERSION AL532233.1 GI:12795726
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 988)
AUTHORS Li, W.B., Gruber, C., Jessup, J. and Polajars, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
bp 191 91006 EVRY cedex France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr.
FEATURES
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/sex="male"
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/lab_host="DH10B"
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was primed with a NotI-Oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact: Peng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Email: filang@lifetech.com URL:
http://fulllength.invitrogen.com"
BASE COUNT 306 a 188 c 242 g 251 t 1 others
ORIGIN
Query Match 15.5% Score 253.4 DB 9: Length 988;
Best Local Similarity 57.1% Pred No. 1.6e-59;
Matches 500; Conservative 0; Mismatches 371; Indels 4; Gaps 2;
Oy 4 GCAGAAAGAAATCAAAATTTTCAGCAGATGCCGCTGCTGCATGTCGCGGAGTATANG 63
Db 115 GCAGAAAGTGAATTTTGTGTCAGATGCCGAGCTTTAATGCTTCAAGGTGATGACTT 174
Oy 64 TTACGATACCGCTCAAGTAAAGCTTGTCTTAAAGGCGCAATGTTCTTGAANA 123
Db 175 TTAGCGATGCTGTGCGCTTACATGCGGCCAAGGAGAAACAGTATATTTGAGCAG 234
Oy 124 GCTTTGGTTCCTCTTATTAATGATGACGGGGTAAACATTTCTTAAAGATGATTA 183
Db 235 AGTTGGGAGAGTCCCAAGTAAACAAAGATGCTGTGACTGTTCACAAATTTGACTTA 294
Oy 184 GAAGATCTTTTAAACATGAGAGCAAAATTTGCTGTAAGTGGCTTTAAACCAAT 243
Db 295 AAAGATTAATCAAAAACATTTGAGTAACTTTGTAAGTTGCTTCCAAATACCAAT 354
Oy 244 GATATGCTGTATGAGAGCACTGACATGTTGATGATGATGATGATGATGATGATG 303
Db 355 GAAAGAGTGGGATGAGCACTACCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTG 414
Oy 304 GCACATAAAATGTGACAGCGTCTATTCATTTGTTTCCGTGAGGCTTGAACA 363
Db 415 GCTTCGAGAAATTTGCAAAAGGCTATTCAGTGAATTCAGAGAGGAGTGTATTA 474
Oy 364 GCACACGCAACAGCTGTGAAGCCTTGAAGCCATTTGCTCAACCTGTATCTGCAAGAA 423
Db 475 GCTGTGATGCTGTATTTGCTGAACCTTAAAGACAGTCTAAACCTGTGACCCCTGAA 534
Oy 424 GCTATGCTAGGTGCTGCTGAGTATCATCAGCTCTGAAAAAG---TTGAGAGTATATC 480
Db 535 GAAATTCACAGAGTGTGCTACGATTTCTGCAACGAGACAAAGAAATTTGCCAATATC 594
Oy 481 TCAGAGCTATGAGAGCTGTGGCAGACGATGATGATGATGATGATGATGATGATG 540
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Db 655 CTGAATGATGAATTTTGAAGATTTTGAAGCATGAAAGTTTGAAGGCTATATTTCTCA 714
Oy 601 TACATGCTCAGACAAATGAAAAATGTTGACAGCTTGAANAACCATTTATCTTAATC 660
Db 715 TACTTTATTAATACATCAAAAGTGCAGAAATGTAATTCAGAGTCCATGATGTTGTG 774
Oy 661 ACGGATAAAAAGTCAACATCCAGACATTTTGCACACTGCTGAGAGTCTTAA 720
Db 775 ACTGTAAGAAATTTTCTAGATTCAGTCCATGCTGCTCTCTTGAATTTGCCATGCT 834
Oy 721 ACCAAGCTCATTTACTATTTGATGATGATGATGATGATGATGATGATGATGATG 780
Db 835 CACGCTAAGCTTGTGCTATTAATGCTGGAAGATGTTGATGAGAAAGCTTAAAGACTC 894
Oy 781 GCTTGAACAAAGTGTGCTGCTCATTTCAATGTTGTTGCTGTAAGGCCAGGATTTGT 840

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Db 895 GTCCTGAAAGAGCTAAAGCTTGTCTTCAGTGTGACGATCAAGCTCCAGGCTTGTGT 954

Qy 841 GATCGTCGTAAGCTATGCTGAAGACATGCTAT 875

Db 955 GACAAATAG-AAAGAACGCTTAAAGATATGCTAT 988

RESULT 13

LOCUS BG321293 977 bp mRNA linear EST 27-FEB-2001

DEFINITION Zm04.04g09_R.Zm04.AAFC_ECORC_cold_stressed_maize_seedlings Zea mays

ACCESSION BG321293

VERSION BG321293.1 GI:13150971

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays.

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.

AUTHORS Singh, J.A., Makui, K., Couroux, P., De Moors, A., Harris, L.J., Hattori, J.I., Ouellet, T., Robert, L.S., Sprott, D. and Tinker, N.A.

TITLE Expressed Sequence Tags from Cold-Stressed Maize Seedlings

JOURNAL Unpublished (2001)

COMMENT Contact: Singh, J.A.

Eastern Cereal and Oilseed Research Centre

Agriculture and Agri-food Canada

KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A 0C6, Canada

Tel: (613) 759-1662

Fax: (613) 759-1701

Email: singh@agr.ca

FEATURES

Location/Qualifiers

source

1..977

/organism="Zea mays"

/cultivar="CO328"

/db_xref="taxon:4577"

/clone="Zm04.04g09"

/clone_11b="Zm04.AAFC_ECORC_cold_stressed_maize_seedlings"

/tissue_type="leaf, crown"

/note="Vector: Bluescript SK-/XhoI-EcoRI; Site 1: Eco RI; Site 2: Xho I; Lower temperature 50 C / hour from 22 to 120C; bring to 50 in 1 hour from 120C. Leave at 50C 2 days , photoperiod 16 hours. Light intensity was 125 uE-1. Library prepared by in vivo mass excision from amplified library."

BASE COUNT 276 a 205 c 241 g 223 t 32 others

ORIGIN

Query Match 15 4% Score 253; DB 13; Length 977;

Best Local Similarity 57.0%; Pred. No. 2, 1e-53;

Matches: 436; Conservative 22; Mismatches 304; Indels 3; Gaps 1;

Qy 4 GCAAGAAATCAATTTTACGACGATGCCGTGTCATGTCGCGAGAGTGCATATG 63

Db 213 GCGAAGACATCAAGTTGTTGAGCCCGTTCCTCCTGTAAGAGGTTGTGAGAG 272

Qy 64 TTACGAGATACCGTCAAGTAAAGCTGTCCTAAAGCCGCAATGTTGTTGAAAA 123

Db 273 TTGGCAGAMGCTTTAAAGTTTAAAGTTGACCTAAGGCGCCCATGKTGTATGACAA 332

Qy 124 GCTTTTGTCTCCTTAATTAATGACGGGGTAAACCATGCTGCTAAAGATGATTA 183

Db 333 AGCTTTKGTGACGAAAGTCAAGAGATGGTTACTTAGCAAAAGCATGATTT 392

Qy 184 GAAGATCAATTTTGAACATGGGAGCAAAATGCTGTGAAGGCTCTTAAACCAAT 243

Db 393 AAGCATAGATTAAGAAATGTTGTCAGAGTTTGAAACAGGTTGTAATGACATTAAT 452

Qy 244 GATTTCTGTGTGGCGACTTACGCAACGTTTTCACACAGCATTTGTCATGAA 303

Db 453 GACACTTCGCGCATGATGACACATGTCACCATCTTTTGAACAAACAAATATTTACTGAG 512

Qy 304 GACATTAATAATTTGACACAGAGTGCTAATTCATTTGATATCCGTGAGGATTAAGA 363

Db 513 GGCTCAAAATCTGTGCGCTGGATTAATGCTAATGATTAAGGCGTGAATCAAG 572

Qy 364 GCAACAGCAACAGCTTTGAAGCCCTTGAAGCCATTTGCTCAACCTGTATCTGCAAGAA 423

Db 573 GCTGTTGACGCTTTGTTACCAATCTTAAARCATGAGCCAGAAATKATCAGACTCAGA 632

Qy 424 GCTATTTGTCAGTCCGTCAGTATCATCAGCTCTGAAGAA-AGTTGAGAGTTATTC 480

Db 633 GAAATTCACAGGTGGGTACAAATATCAGCAATGGGGAAGGCAATTTGTGAGCATT 692

Qy 481 TCAGAGCTATGAGCGTGGGCAAGCATGGTGTGATTCATCAGTAATTCAGAGT 540

Db 693 GCAAGGCTATGAGAGAGTTGGCAAGAGGCTGTATACCTATTTCCGACGTAACAC 752

Qy 541 ATGGAAGCAAGATGATGATGCTGTTGAAGCATGATTCACGCTGTACCTCTCA 600

Db 753 CTTTATATAGCTTTTATGATGAGGTATTAACACTACAGAGTTACATCTCTCG 812

Qy 601 TACATGTCACAGACAAATGAATGTTGCAAGCTTGAAGCCATTTATCTTATTC 660

Db 813 TACTTCATTCACAAACCCAAAGAAATGTAATGGAGACBAYGATCTTAAT 872

Qy 661 ACGATTAATAAGTGTCAACATCCAGACATTTTGCCACTCTTGAGGAATCTTAA 720

Db 873 CATGACAGAGGTGACGACATGATTCATTCGTATGAGAGTTGAAATGCTCTAAG 932

Qy 721 ACCAAGCTCATCTATCTATTTGACATGATGATGATGATGATGATGATGATGAT 765

Db 933 AATCAAAAGCTCTGATGATTTTGCAGAGATGATGATGATGATGATGATGATGAT 977

RESULT 14

LOCUS AL515262 955 bp mRNA linear EST 13-FEB-2001

DEFINITION AL515262 LTI.NFL006.PL2 Homo sapiens CDNA clone CLOB0162A04 5

ACCESSION AL515262

VERSION AL515262.1 GI:12778755

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

Location/Qualifiers

source

1..955

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/db_xref="taxon:9606"

/clone="CLOB0162A04"

/clone_11b="LTI.NFL006.PL2"

/tissue_type="placenta"

/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-ligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 288 a 181 c 236 g 247 t 3 others

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ORIGIN
Query Match      15.4% Score 251.6; DB 9; Length 955;
Best Local Similarity 57.0%; Pred. No. 5e-59;
Matches 480; Conservative 0; Mismatches 359; Indels 3; Gaps 1;

OY 4 GCAGAGAAATCAATTTTACAGAGATGCGGCTGCTGCGGACAGAGTGTATG 63
DB 114 GCAGAGAAATCAATTTTACAGAGATGCGGCTGCTGCGGACAGAGTGTATG 173
OY 64 TTACAGAGATGCGGCTGCTGCGGACAGAGTGTATG 123
DB 174 TTACAGAGATGCGGCTGCTGCGGACAGAGTGTATG 233
OY 124 GCTTTGGTTCCTTAACTAATGAGGAGTGTATG 183
DB 234 AGTGGGAGAGTGTATGAGGAGTGTATG 233
OY 184 GAAGATCAATTTGAAACATGAGGAGTGTATG 243
DB 294 AAAGATCAATTTGAAACATGAGGAGTGTATG 353
OY 244 GATTTGCTGCTGAGGAGTGTATG 303
DB 354 GAAGAGTGTGAGGAGTGTATG 413
OY 304 GCAGTAAATTTGACAGAGTGTATG 363
DB 414 GCCTTGAGAGATTTACAAAGTGTATG 473
OY 364 GCAGAGAGAGTGTATGAGGAGTGTATG 423
DB 474 GCTTTGAGTGTATGAGGAGTGTATG 533
OY 424 GATTTGCTGCTGAGGAGTGTATG 480
DB 534 GAATTTGCTGCTGAGGAGTGTATG 593
OY 481 TCAGAGTGTGAGGAGTGTATG 540
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DB 654 CTGAATGATGATGAGGAGTGTATG 713
OY 601 TACATGCTGACAGAGTGTATG 660
DB 714 TACATGCTGACAGAGTGTATG 773
OY 661 ACAGATTAAGAGTGTATGAGGAGTGTATG 720
DB 774 AGTGAAGAGAGTGTATGAGGAGTGTATG 833
OY 721 ACCAGAGTGTATGAGGAGTGTATG 780
DB 834 CACCTAGAGTGTATGAGGAGTGTATG 893
OY 781 GCTTTGAGAGTGTATGAGGAGTGTATG 840
DB 894 GCTTTGAGAGTGTATGAGGAGTGTATG 953
OY 841 GA 842
DB 954 GA 955

RESULT 15
AL515579 1017 bp mRNA linear EST 13-FEB-2001
LOCUS AL515579
DEFINITION AL515579 LTR1.NFL011.NBC1 Homo sapiens cDNA clone CS0DA002YD20.5
ACCESSION AL515579 prime. mRNA sequence.

VERSION AL515579.1 GI:12779072
KEYWORDS EST.
SOURCE human
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1017)
AUTHORS L.W.B., Gruber, C., Jesse, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Genoscope - Centre National de Sequencage
Contact: BP 191 91006 Evry cedex - France
Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
1. 1017
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/clone_1bp="LTR1.NFL011.NBC1"
/sex="male"
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/1ad_host="DH10B"
/notes="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifestech.com URL: http://fulllength.invitrogen.com"
BASE COUNT 308 a 191 c 255 g 261 t 2 others
ORIGIN
Query Match      15.2% Score 249.6; DB 9; Length 1017;
Best Local Similarity 56.8%; Pred. No. 1.9e-58;
Matches 478; Conservative 1; Mismatches 360; Indels 3; Gaps 1;

OY 4 GCAGAGAAATCAATTTTACAGAGATGCGGCTGCTGCGGACAGAGTGTATG 63
DB 116 GCAGAGAAATCAATTTTACAGAGATGCGGCTGCTGCGGACAGAGTGTATG 175
OY 64 TTACAGAGATGCGGCTGCTGCGGACAGAGTGTATG 123
DB 176 TTACAGAGATGCGGCTGCTGCGGACAGAGTGTATG 233
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OY 184 GAAGATCAATTTGAAACATGAGGAGTGTATG 243
DB 296 AAAGATCAATTTGAAACATGAGGAGTGTATG 355
OY 244 GATTTGCTGCTGAGGAGTGTATG 303
DB 356 GAAGAGTGTGAGGAGTGTATG 413
OY 304 GCAGTAAATTTGACAGAGTGTATG 363
DB 416 GCTTTGAGAGATTTACAAAGTGTATG 473
OY 364 GCAGAGAGAGTGTATGAGGAGTGTATG 423
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OY 424 GATTTGCTGCTGAGGAGTGTATG 480
DB 536 GAATTTGCTGCTGAGGAGTGTATG 595

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Page 14

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Qy	541	ATGGAAACAGAACTGTAAGTGGTTGAAGCATCAATTTGACCGCTGTACCTGGTCCAA	600
Db	656	CTGAATGATGATATAGAAATTATTGTAAGGATGAAGTTGATCGAGCTATATTCTCCA	715
Qy	601	TACATGTGCACAGACAATAAAAAATGTTCGCAGACCTGAAAAACCATTTATCTATATC	660
Db	716	TACTTTATTAATATCAACAAAGCTCAGAAATGTGAATTCACAGATGCGCTATGTTGTG	775
Qy	661	ACGGATATAAAAGTGCACAACATCCAGACATTTTGCCACTACTGTAGGAAGTCTTAA	720
Db	776	ATGTAAAAAGAAATTTCTGATTCACATGTCATTTGTAACCTGCTTGTAAATTCACAAATGCT	835
Qy	721	ACCAACGCTCATTAATGATTTTTCAGATAGATGTGATGTGAAGCACTTCCAAACCTT	780
Db	836	CACCTTAAGCTTTGTGCTATATTCGCTGAAAGATGTGTAGTAGAAGCTTAAATGTAACATC	895
Qy	781	GTCTTGAAACAAGATGTGCTGTACTTTCATATGTGTGCTGTCCAAGCGCAGAGATTTGGT	840
Db	896	GTCTTGAAATGGCTAAAGATGTGTGCTTTCAGAGTTGTGGCAATGAAGGCTCAGAGGTTTGGT	955
Qy	841	GA 842	
Db	956	GA 957	

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